

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: LITTMAN, DAN R.  
DENG, HONGKUI  
ELLMEIER, WILFRIED  
LANDAU, NATHANIEL R.  
LIU, RONG
- (ii) TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH  
MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC  
USES THEREOF
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: David A. Jackson, Esq.  
(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th  
Floor  
(C) CITY: Hackensack  
(D) STATE: New Jersey  
(E) COUNTRY: USA  
(F) ZIP: 07601
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/666,020  
(B) FILING DATE: 19-JUN-1996  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/227,319  
(B) FILING DATE: 13-APR-1994
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Jackson Esq., David A.  
(B) REGISTRATION NUMBER: 26,742  
(C) REFERENCE/DOCKET NUMBER: 1049-1-004 N1
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 201-487-5800

(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 29 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGATCCG GTGGAACAAG ATGGATTAT

29

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 28 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTCGTCGACA TGTGCACAAC TCTGACTG

28

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 66 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGATTATC AAGTGTCAAG TCCAATCTAT GACATCAATT ATTATACATC GGAGCCCTGC

60

CAAAAAA

66

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr  
1 5 10 15

Ser Glu Pro Cys Gln Lys  
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGATTATC AAGTGTC AAG TCCAATCTAT GACATCAATT ATCCATACGA TGTTCCAGAT 60  
TATGCTTCGG AGCCCTGCCA AAAA 84

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Pro Tyr  
1 5 10 15  
Asp Val Pro Asp Tyr Ala Ser Glu Pro Cys Gln Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATCAATTATC CATACGATGT TCCAGATTAT GCTTCGGAGC CCTGCCAAAA A 51

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "Oligonucleotides"

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAGGATCCA CCATGGATTA TCAAGTGTC AAGTCCAATCT ATGACATCAA TTATCCATAC 60

GAT 63

- (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATACGATG TTCCAGATTA TGCT 24

- (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO

- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Tyr Asp Val Pro Asp Tyr Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TATCCATACG ATGTTCCAGA TTATGCTTCG

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3383 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGAAGAGCTG AGACATCCGT TCCCCTACAA GAAACTCTCC CCGGGTGGAA CAAGATGGAT	60
TATCAAGTGT CAAGTCCAAT CTATGACATC AATTATTATA CATCGGAGCC CTGCCAAAAA	120
ATCAATGTGA AGCAAATCGC AGCCCCGCTC CTGCCTCCGC TCTACTCACT GGTGTTTCATC	180
TTTGGTTTGG TGGGCAACAT GCTGGTCATC CTCATCCTGA TAAACTGCAA AAGGCTGAAG	240
AGCATGACTG ACATCTACCT GCTCAACCTG GCCATCTCTG ACCTGTTTTT CCTTCTTACT	300
GTCCCTTCTT GGGCTCACTA TGCTGCCGCC CAGTGGGACT TTGGAAATAC AATGTGTCAA	360
CTCTTGACAG GGCTCTATTT TATAGGCTTC TTCTCTGGAA TCTTCTTCAT CATCCTCCTG	420
ACAATCGATA GGTACCTGGC TGTCGTCCAT GCTGTGTTTG CTTTAAAGC CAGGACGGTC	480
ACCTTTGGGG TGGTGACAAG TGTGATCACT TGGGTGGTGG CTGTGTTTGC GTCTCTCCCA	540
GGAATCATCT TTACCAGATC TCAAAAAGAA GGTCTTCATT ACACCTGCAG CTCTCATTTT	600
CCATACAGTC AGTATCAATT CTGGAAGAAT TTCCAGACAT TAAAGATAGT CATCTTGGGG	660
CTGGTCCTGC CGTGCTTGT CATGGTCATC TGCTACTCGG GAATCCTAAA AACTCTGCTT	720
CGGTGTGCAA ATGAGAAGAA GAGGCACAGG GCTGTGAGGC TTATCTTCAC CATCATGATT	780
GTTTATTTTC TCCTTGGGGC TCCCTACAAC ATTGTCCTTC TCCTGAACAC CTTCCAGGAA	840
TTCTTTGGCC TGAATAATTG CAGTAGCTCT AACAGGTTGG ACCAAGCTAT GCAGGTGACA	900
GAGACTCTTG GGTGACGCA CTGCTGCATC AACCCCATCA TCTATGCCCT TGTCGGGGAG	960
AAGTTCAGAA ACTACCTCTT AGTCTTCTTC CAAAAGCACA TTGCCAAACG CTTCTGCAAA	1020
TGCTGTTCTA TTTTCCAGCA AGAGGCTCCC GAGCGAGCAA GCTCAGTTTA CACCCGATCC	1080
ACTGGGGAGC AGGAAATATC TGTGGGCTTG TGACACGGAC TCAAGTGGGC TGGTGACCCA	1140
GTGACAGTTG TGCACATGGC TTAGTTTICA TACACAGCCT GGGCTGGGGG TGGGGTGGGA	1200
GAGGTCTTTT TTAAGAGGAA GTTACTGTTA TAGAGGTCTT AAGATTATC CATTTATTTG	1260

GCATCTGTTT AAAGTAGATT AGATCTTTTA AGCCCATCAA TTATAGAAAG CCAAATCAAA	1320
ATAITGTGAT GAAAAATAGC AACCTTTTTA TCTCCCTTC ACATGCATCA AGTTATTGAC	1380
AAACTCTCCC TTCACTCCGA AAGTTCCTTA TGTATATTTA AAAGAAAGCC TCAGAGAATT	1440
GCTGATTCTT GAGTTTAGTG ATCTGAACAG AAATACCAAA ATTATTTTCAG AAATGTACAA	1500
CTTTTACCT AGTACAAGGC AACATATAGG TTGTAAATGT GTTTAAACA GGTCTTTGTC	1560
TTGCTATGGG GAGAAAGAC ATGAATATGA TTAGTAAAGA AATGACACTT TTCATGTGTG	1620
ATTTCCTTC CAAGGTATGG TTAATAAGTT TCACTGACTT AGAACCAGGC GAGAGACTTG	1680
TGGCTGGGA GAGCTGGGA AGCTTCTTAA ATGAGAAGGA ATTTGAGTTG GATCATCTAT	1740
TGCTGGCAA GACAGAAGCC TCACTGCAAG CACTGCATGG GCAAGCTTGG CTGTAGAAGG	1800
AGACAGAGCT GGTGGGAAG ACATGGGGAG GAAGGACAAG GCTAGATCAT GAAGAACCCT	1860
GACGCGATTG CTCCGCTTAA GTCATGAGCT GAGCAGGAG ATCCTGTTG GTGTTGCAGA	1920
AGGTTTACTT TGTGGCCAAA GGAGGGTCAG GAAGGATGAG CATTTAGGGC AAGGAGACCA	1980
CCAACAGCCC TCAGGTCAGG GTGAGGATGG CCTCTGCTAA GCTCAAGGCG TGAGGATGGG	2040
AAGGAGGGAG GTATTCTGTA GGTATGGGAAG GAGGGAGGTA TTCGTGCAGC ATATGAGGAT	2100
GCAGAGTCAG CAGAACTGGG GTGGATTGG TTTGGAAGTG AGGGTCAGAG AGGAGTCAGA	2160
GAGAATCCCT AGTCTTCAAG CAGATTGGAG AAACCCCTTA AAAGACATCA AGCACAAGAAG	2220
GAGGAGGAGG AGGTTTAGGT CAAGAAGAAG ATGGATTGGT GTAAAAGGAT GGGTCTGGTT	2280
TGCAGAGCTT GAACACAGTC TCACCCAGAC TCCAGGCTGT CTTTCACTGA ATGCTTCTGA	2340
CTTCATAGAT TTCCTTCCA TCCAGCTGA AATACTGAGG GGTCTCCAGG AGGAGACTAG	2400
ATTTATGAAT ACACGAGGTA TGAGGTCTAG GAACATACTT CAGCTCACAC ATGAGATCTA	2460
GGTGAGGATT GATTACCTAG TAGTCATTTT ATGGTTGTT GGGAGGATTC TATGAGGCAA	2520
CCACAGGCGC CATTTAGCAC ATACTACACA TTCAATAAGC ATCAAATCTT TAGTTACTCA	2580
TTCAAGGATA GCACTGAGCA AAGCATTGAG CAAAGGGGTC CCATATAGGT GAGGGAAGCC	2640
TGAAAACTA AGATGCTGCC TGCCCCAGTC ACACAAGTGT AGGTATCATT TTCTGCATTT	2700
AACCGTCAAT AGGCAAAGGG GGAAGGGGAC ATATTCACTT GGAATAAGC TGCCCTGAGC	2760
CTTAAACCC ACAAAAGTAC AATTTACCAG CCTCCGTATT TCAGACTGAA TGGGGGTGGG	2820
GGGGCGCCT TAGGTACTTA TTCCAGATGC CTTCTCAGA CAAACCAGAA GCAACAGAAA	2880
AAATCGTCTC TCCCTCCCTT TGAAATGAAT ATACCCCTTA GTGTTTGGGT ATATTCACTT	2940



CAAAGGGAGA GAGAGAGGTT TTTTCTGTT CTTTCTCATA TGATTGTGCA CATACTTGAG 3000  
 ACTGTTTTGA ATTTGGGGGA TGGCTAAAC CATCATAGTA CAGGTAAGGT GAGGGAATAG 3060  
 TAAGTGGTGA GAACTACTCA GGAATGAAG GTGTCAGAAT AATAAGAGGT GCTACTGACT 3120  
 TTCTCAGCCT CTGAATATGA ACGGTGAGCA TTGTGGCTGT CAGCAGGAAG CAACGAAGGG 3180  
 AAATGICTTT CTTTTCGCTC TTAAGTTGTG GAGAGTGCAA CAGTAGCATA GGACCCCTACC 3240  
 CTCTGGGCCA AGTCAAAGAC ATTCTGACAT CTTAGTATTT GCATATTCTT ATGTATGTGA 3300  
 AAGTTACAAA TTGCTTGAAA GAAAATATGC ATCTAATAAA AACACCTTC TAAATAAAAA 3360  
 AAAAAAAAAA AAAAAAAAAA AAA 3383

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr	Thr
1				5					10				15		
Ser	Glu	Pro	Cys	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu
			20				25						30		
Leu	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn
			35				40					45			
Met	Leu	Val	Ile	Leu	Ile	Leu	Ile	Asn	Cys	Lys	Arg	Leu	Lys	Ser	Met
	50					55					60				
Thr	Asp	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Phe	Phe	Leu
65					70					75				80	
Leu	Thr	Val	Pro	Phe	Trp	Ala	His	Tyr	Ala	Ala	Ala	Gln	Trp	Asp	Phe
				85					90					95	
Gly	Asn	Thr	Met	Cys	Gln	Leu	Leu	Thr	Gly	Leu	Tyr	Phe	Ile	Gly	Phe
			100					105						110	

Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu  
 115 120 125  
 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe  
 130 135 140  
 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser  
 145 150 155 160  
 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr  
 165 170 175  
 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn  
 180 185 190  
 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu  
 195 200 205  
 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys  
 210 215 220  
 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile  
 225 230 235 240  
 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu  
 245 250 255  
 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser  
 260 265 270  
 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr  
 275 280 285  
 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe  
 290 295 300  
 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe  
 305 310 315 320  
 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser  
 325 330 335  
 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu  
 340 345 350